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RAW SEQUENCE LISTING   DATE: 01/15/2003 *P.6*
PATENT APPLICATION: **US/10/081,301A**   TIME: 09:40:44

Input Set : **A:\BB-1201 US DIV Corrected Sequence Listing.txt**
Output Set: **N:\CRF4\01152003\J081301A.raw**

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TECH CENTER 1600/2900

```
 3 <110> APPLICANT: Falco, S. Carl
 4        Cahoon, Rebecca E.
 7 <120> TITLE OF INVENTION: Vitamin B Metabolism Proteins
 9 <130> FILE REFERENCE: BB-1201 US DIV
11 <140> CURRENT APPLICATION NUMBER: 10/081,301A
12 <141> CURRENT FILING DATE: 2002-02-20
14 <150> PRIOR APPLICATION NUMBER: 60/096,342
15 <151> PRIOR FILING DATE: 1998-08-12
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: Microsoft Office 97
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 933
23 <212> TYPE: DNA
24 <213> ORGANISM: Zea mays
26 <400> SEQUENCE: 1
27 atggcgcggc cgccgatcct atccgtcgcg ctgccgtctg acaccggccg tgtgctcagc  60
28 atccagtccc acaccgtcca ggggtatgtt ggcaacaaat cggccgtctt tcccctgcag 120
29 ctccttggct ttgatgtgga tccaataaac tctgtacagt tttctaatca tacaggatac 180
30 ccaacattta gaggtcaggt tcttaatggc aaacagctct gggaccttat tgaaggactg 240
31 gaggaaaatc agttgcttca ttatacccat ttattaacag gttatatagg ctcagtttcc 300
32 tttttagata ctgtgctaca agttgttgag aaattgcgat cagttaatcc tgatcttgta 360
33 tatgtttgtg acccagttct aggtgatgaa ggaaaactat atgttcctca ggaggtaata 420
34 tctgtttatc aacagaaggt tgttccagtt gcttcaatgc ttacacctaa ccaatttgaa 480
35 gttgaactac ttactggatt gaggatcacc tccgaagaag atggtttgac agcttgtaat 540
36 accctccaca gtgccggacc acagaaggtg gttataacta gtgctcttat tgaaggtaag 600
37 ctgctcctta tcggaagtca caaaaaaaca gaggaacaac agccagaaca atttaagatt 660
38 gagataccaa agatacctgc atatttcacg ggaactggag atttgacaac tgctctccta 720
39 ctaggatgga gtaataaata tcctgatagc ctcgagaaag cagcagaact ggcagtttcc 780
40 agtttgcagg cacttctgaa aagaactgtg gaagactata aaatggccgg cttcgaccca 840
41 tcgaccagca gcttagagat ccggttgatc caaagccagg acgagatccg aaacccaact 900
42 gttacatgca aggctgtgaa gtatggaagc tga                               933
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 310
46 <212> TYPE: PRT
47 <213> ORGANISM: Zea mays
49 <400> SEQUENCE: 2
50 Met Ala Arg Pro Pro Ile Leu Ser Val Ala Leu Pro Ser Asp Thr Gly
51  1               5                  10                  15
53 Arg Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn
54              20                  25                  30
56 Lys Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Phe Asp Val Asp Pro
57          35                  40                  45
59 Ile Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Arg
```

```
60       50                        55                    60
62 Gly Gln Val Leu Asn Gly Lys Gln Leu Trp Asp Leu Ile Glu Gly Leu
63   65                    70                 75                 80
65 Glu Glu Asn Gln Leu Leu His Tyr Thr His Leu Leu Thr Gly Tyr Ile
66                 85                 90                 95
68 Gly Ser Val Ser Phe Leu Asp Thr Val Leu Gln Val Val Glu Lys Leu
69            100                105                110
71 Arg Ser Val Asn Pro Asp Leu Val Tyr Val Cys Asp Pro Val Leu Gly
72            115                120                125
74 Asp Glu Gly Lys Leu Tyr Val Pro Gln Glu Val Ile Ser Val Tyr Gln
75      130               135                140
77 Gln Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu
78 145                150                155                160
80 Val Glu Leu Leu Thr Gly Leu Arg Ile Thr Ser Glu Glu Asp Gly Leu
81                165                170                175
83 Thr Ala Cys Asn Thr Leu His Ser Ala Gly Pro Gln Lys Val Val Ile
84            180                185                190
86 Thr Ser Ala Leu Ile Glu Gly Lys Leu Leu Leu Ile Gly Ser His Lys
87            195                200                205
89 Lys Thr Glu Glu Gln Gln Pro Glu Gln Phe Lys Ile Glu Ile Pro Lys
90      210                215                220
92 Ile Pro Ala Tyr Phe Thr Gly Thr Gly Asp Leu Thr Thr Ala Leu Leu
93 225                230                235                240
95 Leu Gly Trp Ser Asn Lys Tyr Pro Asp Ser Leu Glu Lys Ala Ala Glu
96                245                250                255
98 Leu Ala Val Ser Ser Leu Gln Ala Leu Leu Lys Arg Thr Val Glu Asp
99            260                265                270
101 Tyr Lys Met Ala Gly Phe Asp Pro Ser Thr Ser Ser Leu Glu Ile Arg
102      275                280                285
104 Leu Ile Gln Ser Gln Asp Glu Ile Arg Asn Pro Thr Val Thr Cys Lys
105      290               295                300
107 Ala Val Lys Tyr Gly Ser
108 305               310
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 413
112 <212> TYPE: DNA
113 <213> ORGANISM: Oryza sativa
115 <220> FEATURE:
116 <221> NAME/KEY: unsure
117 <222> LOCATION: (380)
118 <223> OTHER INFORMATION: n = a, c, g or t
120 <220> FEATURE:
121 <221> NAME/KEY: unsure
122 <222> LOCATION: (384)
123 <223> OTHER INFORMATION: n = a, c, g or t
125 <220> FEATURE:
126 <221> NAME/KEY: unsure
127 <222> LOCATION: (388)
128 <223> OTHER INFORMATION: n = a, c, g or t
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RAW SEQUENCE LISTING   DATE: 01/15/2003
PATENT APPLICATION: US/10/081,301A   TIME: 09:40:44

Input Set : A:\BB-1201 US DIV Corrected Sequence Listing.txt
Output Set: N:\CRF4\01152003\J081301A.raw

```
130 <220> FEATURE:
131 <221> NAME/KEY: unsure
132 <222> LOCATION: (410)
133 <223> OTHER INFORMATION: n = a, c, g or t
135 <400> SEQUENCE: 3
136 gtttaaacaa gaagatggct tgaaagcttg caatgcgcta catagtgctg gaccgcgaaa   60
137 ggtggtaata actagtgcac ttattgaaga taagctgctc ctcattggaa gccacaaaaa  120
138 agcaaaggaa caaccaccag aacaatttaa gattgagata cccaagatac ctgcatattt  180
139 cacgggcact ggagatttaa caactgccct tctactagga tggagtaata aataccctga  240
140 taaccttgga gagggcgctg aactggcggt atccatttgc aaggcacccc taaggagaac  300
141 tgtggaagac tataaaagac tgggtttgac cctccaacca acacctagag atccgcctgg  360
W--> 142 attcaaaacc aaggatgaan tccnaagncc caagatacat gcaagctgtn aaa         413
144 <210> SEQ ID NO: 4
145 <211> LENGTH: 136
146 <212> TYPE: PRT
147 <213> ORGANISM: Oryza sativa
149 <220> FEATURE:
150 <221> NAME/KEY: UNSURE
151 <222> LOCATION: (127)..(128)..(129)
152 <223> OTHER INFORMATION: Xaa = any amino acid
154 <400> SEQUENCE: 4
155 Phe Lys Gln Glu Asp Gly Leu Lys Ala Cys Asn Ala Leu His Ser Ala
156  1               5                  10                  15
158 Gly Pro Arg Lys Val Val Ile Thr Ser Ala Leu Ile Glu Asp Lys Leu
159              20                  25                  30
161 Leu Leu Ile Gly Ser His Lys Lys Ala Lys Glu Gln Pro Pro Glu Gln
162          35                  40                  45
164 Phe Lys Ile Glu Ile Pro Lys Ile Pro Ala Tyr Phe Thr Gly Thr Gly
165      50                  55                  60
167 Asp Leu Thr Thr Ala Leu Leu Leu Gly Trp Ser Asn Lys Tyr Pro Asp
168  65                  70                  75                  80
170 Asn Leu Gly Glu Gly Ala Glu Leu Ala Val Ser Ile Cys Lys Ala Pro
171              85                  90                  95
173 Leu Arg Arg Thr Val Glu Asp Tyr Lys Arg Leu Gly Leu Thr Leu Gln
174             100                 105                 110
W--> 176 Pro Thr Pro Arg Asp Pro Pro Gly Phe Lys Thr Lys Asp Glu Xaa Xaa
177             115                 120                 125
W--> 179 Xaa Pro Lys Ile His Ala Ser Cys
180         130                 135
182 <210> SEQ ID NO: 5
183 <211> LENGTH: 812
184 <212> TYPE: DNA
185 <213> ORGANISM: Glycine max
187 <220> FEATURE:
188 <221> NAME/KEY: unsure
189 <222> LOCATION: (577)
190 <223> OTHER INFORMATION: n = a, c, g or t
192 <220> FEATURE:
193 <221> NAME/KEY: unsure
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/081,301A**

DATE: 01/15/2003
TIME: 09:40:44

Input Set : **A:\BB-1201 US DIV Corrected Sequence Listing.txt**
Output Set: **N:\CRF4\01152003\J081301A.raw**

```
194 <222> LOCATION: (610)
195 <223> OTHER INFORMATION: n = a, c, g or t
197 <220> FEATURE:
198 <221> NAME/KEY: unsure
199 <222> LOCATION: (683)
200 <223> OTHER INFORMATION: n = a, c, g or t
202 <220> FEATURE:
203 <221> NAME/KEY: unsure
204 <222> LOCATION: (687)
205 <223> OTHER INFORMATION: n = a, c, g or t
207 <220> FEATURE:
208 <221> NAME/KEY: unsure
209 <222> LOCATION: (742)
210 <223> OTHER INFORMATION: n = a, c, g or t
212 <220> FEATURE:
213 <221> NAME/KEY: unsure
214 <222> LOCATION: (744)
215 <223> OTHER INFORMATION: n = a, c, g or t
217 <220> FEATURE:
218 <221> NAME/KEY: unsure
219 <222> LOCATION: (746)
220 <223> OTHER INFORMATION: n = a, c, g or t
222 <220> FEATURE:
223 <221> NAME/KEY: unsure
224 <222> LOCATION: (755)
225 <223> OTHER INFORMATION: n = a, c, g or t
227 <220> FEATURE:
228 <221> NAME/KEY: unsure
229 <222> LOCATION: (760)
230 <223> OTHER INFORMATION: n = a, c, g or t
232 <220> FEATURE:
233 <221> NAME/KEY: unsure
234 <222> LOCATION: (769)
235 <223> OTHER INFORMATION: n = a, c, g or t
237 <220> FEATURE:
238 <221> NAME/KEY: unsure
239 <222> LOCATION: (778)
240 <223> OTHER INFORMATION: n = a, c, g or t
242 <220> FEATURE:
243 <221> NAME/KEY: unsure
244 <222> LOCATION: (785)..(786)
245 <223> OTHER INFORMATION: n = a, c, g or t
247 <220> FEATURE:
248 <221> NAME/KEY: unsure
249 <222> LOCATION: (792)
250 <223> OTHER INFORMATION: n = a, c, g or t
252 <220> FEATURE:
253 <221> NAME/KEY: unsure
254 <222> LOCATION: (804)
```

Input Set : A:\BB-1201 US DIV Corrected Sequence Listing.txt
Output Set: N:\CRF4\01152003\J081301A.raw

```
255 <223> OTHER INFORMATION: n = a, c, g or t
257 <400> SEQUENCE: 5
258 gcacgaggag cattttccgg gcacgaaact cgaggaattc gcgcatggcg cctccaatcc  60
259 tctcgctcgc tcttccctcg aacaccggtc gagttctcag cattcaatct cacaccgttc 120
260 aggggtatgt tggtaataaa tccgctgtct tccctctgca actactggga tatgatgtcg 180
261 atccaattaa ttccgtgcag ttttcgaatc atacaggata tccgacgttt aagggtcagg 240
262 ttttgaatgg acagcaactc tgggatctaa tcgaaggcct tgaaggaaat gatttattgt 300
263 tctatactca cttgctaaca ggttatattg gttcagagtc ttttctaaac actgtattgc 360
264 aagttgtcag caaacttcgg tcaacaaacc caggtctttc gtatgtatgt gatccagtga 420
265 tgggtgatga aggaaagctt tatgttcctc aagagctagt atcagtctat cgtgagaagg 480
266 ttgttccagt agcttcaatg ttgactccca accagtttga agcagaacta ctgacaggct 540
W--> 267 ttaggattca gtctgaagga catggccggg aggctgntag gcttctccat gcagctgggc 600
W--> 268 cttcaaaggn cataattaca agtataaata tagacgggat tcttctcctc attggcagtc 660
W--> 269 atccaaaaga aaagggagag ccncccngac aatttaagat tgttattcca aaaataacca 720
W--> 270 gcttatttta cgggaacggg anancncatg actgnattcn tcttggttng agcataanta 780
W--> 271 cccannacaa ancttgagaa tgcngcggaa ct                                812
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 196
275 <212> TYPE: PRT
276 <213> ORGANISM: Glycine max
278 <220> FEATURE:
279 <221> NAME/KEY: UNSURE
280 <222> LOCATION: (178)
281 <223> OTHER INFORMATION: Xaa = any amino acid
283 <220> FEATURE:
284 <221> NAME/KEY: UNSURE
285 <222> LOCATION: (189)
286 <223> OTHER INFORMATION: Xaa = any amino acid
288 <400> SEQUENCE: 6
289 Met Ala Pro Pro Ile Leu Ser Leu Ala Leu Pro Ser Asn Thr Gly Arg
290  1               5                  10                  15
292 Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn Lys
293             20                  25                  30
295 Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Tyr Asp Val Asp Pro Ile
296         35                  40                  45
298 Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Lys Gly
299     50                  55                  60
301 Gln Val Leu Asn Gly Gln Gln Leu Trp Asp Leu Ile Glu Gly Leu Glu
302 65                  70                  75                  80
304 Gly Asn Asp Leu Leu Phe Tyr Thr His Leu Leu Thr Gly Tyr Ile Gly
305                 85                  90                  95
307 Ser Glu Ser Phe Leu Asn Thr Val Leu Gln Val Val Ser Lys Leu Arg
308             100                 105                 110
310 Ser Thr Asn Pro Gly Leu Ser Tyr Val Cys Asp Pro Val Met Gly Asp
311             115                 120                 125
313 Glu Gly Lys Leu Tyr Val Pro Gln Glu Leu Val Ser Val Tyr Arg Glu
314         130                 135                 140
316 Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu Ala
317 145                 150                 155                 160
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/15/2003
PATENT APPLICATION: US/10/081,301A   TIME: 09:40:45

Input Set : A:\BB-1201 US DIV Corrected Sequence Listing.txt
Output Set: N:\CRF4\01152003\J081301A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 380,384,388,410
Seq#:4; Xaa Pos. 127,128,129
Seq#:5; N Pos. 577,610,683,687,742,744,746,755,760,769,778,785,786,792,804
Seq#:6; Xaa Pos. 178,189
Seq#:9; N Pos. 74
Seq#:10; Xaa Pos. 25
Seq#:11; N Pos. 220,249,353,356,382,388,393,426,430,434,437,473,475,502,506
Seq#:11; N Pos. 519,524,532,536,537,545,549,551
Seq#:12; Xaa Pos. 74,83

VERIFICATION SUMMARY   DATE: 01/15/2003
PATENT APPLICATION: **US/10/081,301A**   TIME: 09:40:45

Input Set : **A:\BB-1201 US DIV Corrected Sequence Listing.txt**
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```
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:360
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:112
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:128
L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:540
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:600
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:660
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:720
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:780
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:176
L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:60
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:180
L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:240
L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:300
L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:360
L:616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:420
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:480
L:618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:540
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:64
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:80
```